

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: PIG IMPROVEMENT COMPANY UK LIMITED
(B) STREET: 100 GEORGE STREET
(C) CITY: LONDON
(D) STATE: LONDON
(E) COUNTRY: ENGLAND
(F) POSTAL CODE (ZIP): W1H 5RH

(A) NAME: ANDERSSON, LEIF
(B) STREET: MELICA HB
(C) CITY: BERGAGATAN 30
(D) STATE: UPPSALA
(E) COUNTRY: SWEDEN
(F) POSTAL CODE (ZIP): S-752 39

(ii) TITLE OF INVENTION: METHODS FOR ANALYSING ANIMAL PRODUCTS

(iii) NUMBER OF SEQUENCES: 50

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB98/01531

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGTAAAACGA CGGCCAGTRG TGCCTGGAGG TGT

33

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER MSHR REVERSE 5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CGCCCAGATG GCCGCGATGG ACCG

24

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CGGCCATCTG GCGGGCAGC GTGC

24

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGAAGGCGTA GATGAGGGGG TCCA

24

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCACATCGCC CGGCTCCACA AGAC

24

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER MSHR REVERSE 3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGGGCAGAGG ACGACGAGGG AGAG

24

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER LA93"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GAGCAGCCCC TACCCCGGAA TGCCAGTTGA

30

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER KIT56"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CTTTAAACA GAACATAAAA GCGGAAACAT CATGCGAAGG

40

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CGCCCAGATG GCCGCGATGG ACCG

24

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TGCGCTACCA CAGCATCGTG ACCCTGC

27

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTAGTAGGCG ATGAAGAGCG TGCT

24

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CTGCCTGGCC GTGTCGGACC TG

22

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CTGTGGTAGC GCAGCGCGTA GAAG

24

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TGAGGTAGGA GAGTTTGGG

20

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TCGAAATTGA GGGGAAGACC

20

- (2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GTATTCACAG AGACTTGGCG GC

22

- (2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAACCTGCAA GGAAAATCCT TCACGG

26

- (2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GAATATTGTT GCTATGGTGA TCTCC

25

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CCGCTTCTGC GTGATCTTCC TG

22

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CTGGATGTCC TGTGTTCCCT GT

22

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AGGTTTGTCT GCAGCAGAAG CTC

23

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GAAAGTGAYG TCTGGTCCTA TSGGAT

26

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AGCCTTCCTT GATCATCTTG TAG

23

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TGTGGGAGCT CTTCTCTTTA GG

22

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CCAGCAGGAC AATGGGAACA TCT

23

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGCTCTGGGG GCTCGGCTTT GC

22

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TCAGACATCT TCGTGGACAA GCAGAGG

27

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TCRTACATAG AAAGAGAYGT GACTC

25

- (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AGCCTTCCTT GATCATCTTG TAG

23

- (2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GAGCAGCCCC TACCCCGGAA TGCCAGTTGA

30

- (2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CTTTAAAACA GAACATAAAA GCGGAAACAT CATGCGAAGG

40

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GGTCTAGATC ACCAGGAGCA CTGCAGCACC

30

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GGGAAGCTTG ACCCCCGAGA GCGACGCGCC

30

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GGACTCCATG GAGCCGCAGA TGAGCACGGT

30

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GCAAGACCCT CCAGGAGGTG

20

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CACTGAGCCG TAGAAGAGAG

20

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 863 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..863
- (D) OTHER INFORMATION:/note= "Fig 1 - Wildboar"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CTCCCTGCTC CCTGCTCCCT GGC GGGACGA TGCCTGTGCT TGGCCCGGAG AGGAGGCTGC	60
TGGCTTCCCT CAGCTCCGCG CCCCAGCCG CCCCCGGCC GCCAACGCCT CGGGCTCAGA	120
CCAACCAGAC GGGCCCCCAG TGCCTGGAGG TGTCCATTCC CGACGGGCTC TTCCTCAGCC	180
TGGGGCTGGT GAGCCTCGTG GAGAACGTGC TGGTGGTGGC CGCCATCGCC AAGAACCGCA	240
ACCTGCACTC GCCCATGTAC TACTTCGTCT GCTGCC TGGC CGTGTCGGAC CTGCTGGTGA	300
GCGTGAGCAA CGTGCTGGAG ACGGCCGTGC TGCTGCTGCT GGAGGCGGGC GCCCTGGCCG	360
CCCAGGCCGC CGTGGTGCAG CAGCTGGACA ATGTCATGGA CGTGCTCATC TGCGGCTCCA	420
TGGTGTCCAG CCTCTGCTTC CTGGGCGCCA TCGCCGTGGA CCGCTACGTG TCCATCTTCT	480
ACGCGCTGCG CTACCACAGC ATCGTGACGC TGCCCCGCGC GGGGCGGGCT ATCGCGGCGA	540
TCTGGGCGGG CAGCGTGCTC TCCGTCAGCT TCTTCGTGGC CATGCTGGCG CTCATGGCGG	600
TACTGTACGT CCACATGCTG GCCCGGGCCT GCCAGCACGG CCGGCACATC GCCCGGCTCC	660
ACAAGACGCA GCACCCACC CGCCAGGGCT GCGGCCTCAA GGGCGCGGCC ACCCTCACCA	720
TCCTGCTGGG CGTCTTCCTC CTCTGCTGGG CACCCTTCTT CCTGCACCTC TCCCTCGTCG	780
TCCTCTGCCC CCAGCACCCC ACCTGCGGCT GCGTCTTCAA GAACGTCAAC CTCTTTCTGG	840
CCCTCGTCAT CTGCAACTCC ATC	863

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 863 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..705
- (D) OTHER INFORMATION: /note= "Fig 1 - Meishan"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CTCCCTGCTC CCTGCTCCCT GGC GGGACGA TGCCTGTGCT TGGCCCGGAG AGGAGGCTGC	60
TGGCTTCCCT CAGCTCCGCG CCCCAGCCG CCCCCGGCC GCCAACGCCT CGGGCTCAGA	120
CCAACCAGAC GGGCCCCCAG TGCCTGGAGG TGTCCATTCC CGACGGGCTC TTCCTCAGCC	180

TGGGGCTGGT GAGCCTCGTG GAGAACGTGC TGGTGGTGGC CGCCATCGCC AAGAACCGCA	240
ACCTGCACTC GCCCATGTAC TACTTCGTCT GCTGCCTGGC CGTGTCTGGAC CTGCTGGTGA	300
GCGTGAGCAA CATGCTGGAG ACGGCCGTGC TGCCGCTGCT GGAGGCGGGC GCCCTGGCCG	360
CCCAGGCCGC CGTGGTGCAG CAGCTGGACA ACGTCATGGA CGTGCTCATC TCGGGCTCCA	420
TGGTGTCCAG CCTCTGCTTC CTGGGCGCCA TCGCCGTGGA CCGCTACGTG TCCATCTTCT	480
ACGCGCTGCG CTACCACAGC ATCGTGACGC TGCCCCGCGC GGGGCGGGCT ATCGCGGCGA	540
TCTGGGCGGG CAGCGTGCTC TCCGTACAGT TCTTCGTGGC CATGCTGGCG CTCATGGCGG	600
TACTGTACGT CCACATGCTG GCCCGGGCCT GCCAGCACGG CCGGCACATC GCCCGGCTCC	660
ACAAGACGCA GCACCCACC CGCCAGGGCT GCGGCCTCAA GGGCGCAGCC ACCCTCACCA	720
TCCTGCTGGG CGTCTTCCTC CTCTGCTGGG CACCCTTCTT CCTGCACCTC TCCCTCGTCG	780
TCCTCTGCCC CCAGCACCCC ACCTGCGGCT GCGTCTTCAA GAACGTCAAC CTCTTTCTGG	840
CCCTCGTCAT CTGCAACTCC ATC	863

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..705
- (D) OTHER INFORMATION:/note= "Fig 1 - Pietrain"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTCCCTGCTC CTTGCTCCCT GGCAGGACGA TGCCTGTGCT TGGCCCGGAG AGGAGGCTGC	60
TGGCTTCCCT CAGCTCCGCG CCCCCAGCCG CCCCCCCC GG CCGCCAACGC CTCGGGCTCA	120
GACCAACCAG ACGGGCCCCC AGTGCCCTGGA GGTGTCCATT CCCGACGGGC TCTTCCTCAG	180
CCTGGGGCTG GTGAGCCTCG TGGAGAACGT GCTGGTGGTG GCCGCCATCG CCAAGAACCG	240
CAACCTGCAC TCGCCCATGT ACTACTTCGT CTGCTGCCTG GCCGTGTCGG ACCTGCTGGT	300
GAGCGTGAGC AACGTGCTGG AGACGGCCGT GCTGCTGCTG CTGGAGGCGG GCGCCCTGGC	360
CGCCAGGCC GCCGTGGTGC AGCAGCTGGA CAATGTCATG AACGTGCTCA TCTGCGGCTC	420

CATGGTGTCC AGCCTCTGCT TCCTGGGCGC CATCGCCGTG GACCGCTACG TGTCCATCTT	480
CTACGCGCTG CGCTACCACA GCATCGTGAC GCTGCCCCGC GCGGGGCGGG CTATCGCGGC	540
GATCTGGGCG GGCAGCGTGC TCTCCGTCAG CTTCTTCGTG GCCATGCTGG CGCTCATGGC	600
GGTACTGTAC GTCCACATGC TGGCCCGGGC CTGCCAGCAC GGCCGGCACA TCGCCCGGCT	660
CCACAAGACG CAGCACCCCA CCCGCCAGGG CTGCGGCCTC AAGGGCGCGG CCACCCTCAC	720
CATCCTGCTG GGCCTCTTCC TCCTCTGCTG GGCACCCTTC TTCTGCACC TCTCCCTCGT	780
CGTCCTCTGC CCCCAGCACC CCACCTGCGG CTGCGTCTTC AAGAACGTCA ACCTCTTTCT	840
GGCCCTCGTC ATCTGCAACT CCATC	865

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..705
- (D) OTHER INFORMATION:/note= "Fig 1 - Largewhite"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CCCACGGGC TCTTCCTCAG CCTGGGGCTG GTGAGCCTCG TGGAGAACGT GCTGGTGGTG	60
GCCGCCATCG CCAAGAACCG CAACCTGCAC TCGCCCATGT ACTACTTCGT CTGCTGCCTG	120
GCCGTGTCGG ACCTGCTGGT GAGCGTGAGC AACGTGCTGG AGACGGCCGT GCTGCTGCTG	180
CTGGAGGCGG GCGCCCTGGC CGCCCAGGCC GCCGTGGTGC AGCAGCTGGA CAATGTCATG	240
AACGTGCTCA TCTGCGGCTC CATGGTGTCC AGCCTCTGCT TCCTGGGCGC CATCGCCGTG	300
GACCGCTACG TGTCCATCTT CTACGCGCTG CGCTACCACA GCATCGTGAC GCTGCCCCGC	360
GCGGGGCGGG CTATCGCGGC GATCTGGGCG GGCAGCGTGC TCTCCGTCAG CTTCTTCGTG	420
GCCATGCTGG CGCTCATGGC GGTACTGTAC GTCCACATGC TGGCCCGGGC CTGCCAGCAC	480
GGCCGGCACA TCGCCCGGCT CCACAAGACG CAGCACCCCA CCCGCCAGGG CTGCGGCCTC	540
AAGGGCGCGG CCACCCTCAC CATCCTGCTG GGCCTCTTCC TCCTCTGCTG GGCACCCTTC	600
TTCTGCACC TCTCCCTCGT CGTCCTCTGC CCCCAGCACC CCACCTGCGG CTGCGTCTTC	660

AAGAACGTCA ACCTCTTTCT GGCCCTCGTC ATCTGCAACT CCATC

705

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..708
- (D) OTHER INFORMATION:/note= "Fig 1 - Hampshire"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATTCCCGACG GGCTCTTCCT CAGCCTGGGG CTGGTGAGCC TCGTGGAGAA CGTGCTGGTG	60
GTGGCCGCCA TCGCCAAGAA CCGCAACCTG CACTCGCCCA TGTACTACTT CGTCTGCTGC	120
CTGGCCGTGT CGGACCTGCT GGTGAGCGTG AGCAACGTGC TGGAGACGGC CGTGCTGCTG	180
CTGCTGGAGG CGGGCGCCCT GGCCGCCAG GCCGCCGTGG TGCAGCAGCT GGACAATGTC	240
ATGAACGTGC TCATCTGCGG CTCCATGGTG TCCAGCCTCT GCTTCCTGGG CGCCATCGCC	300
GTGGACCGCT ACGTGTCCAT CTTCTACGCG CTGCGCTACC ACAGCATCGT GACGCTGCCC	360
CGCGCGGGGC GGGCTATCGC GCGGATCTGG GCGGGCAGCG TGCTCTCCGT CAGCTTCTTC	420
GTGGCCATGC TGGCGCTCAT GGCGGTACTG TACGTCCACA TGCTGGCCCG GGCCTGCCAG	480
CACGGCCGGC ACATCGCCCG GCTCCACAAG ACGCAGCACC CCACCCGCCA GGGCTGCGGC	540
CTCAAGGGCG CGGCCACCCT CACCATCCTG CTGGGCGTCT TCCTCCTCTG CTGGGCACCC	600
TTCTTCCTGC ACCTCTCCCT CGTCGTCCTC TGCCCCAGC ACCCCACCTG CGGCTGCGTC	660
TTCAAGAACG TCAACCTCTT TCTGGCCCTC GTCATCTGCA ACTCCATC	708

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:1..708
- (D) OTHER INFORMATION:/note= "Fig 1 - Duroc"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```
ATTCCCGACG GGCTCTTCCT CAGCCTGGGG CTGGTGAGCC TCGTGGAGAA CGTGCTGGTG      60
GTGGCCGCCA TCGCCAAGAA CCGCAACCTG CACTCGCCCA TGTACTACTT CGTCTGCTGC      120
CTGGCCGTGT CGGACCTGCT GGTGAGCGTG AGCAACGTGC TGGAGACGGC CGTGCTGCTG      180
CTGCTGGAGG CGGGCGCCCT GGCCGCCCAG GCCGCCGTGG TGCAGCAGCT GGACAATGTC      240
ATGGACGTGC TCATCTGCGG CTCCATGGTG TCCAGCCTCT GCTTCCTGGG CGCCATCGCC      300
GTGGACCGCT ACGTGTCCAT CTTCTACGCG CTGCGCTACC ACAGCATCGT GACGCTGCCC      360
CGCGTGGGGC GGGCTATCGC GCGGATCTGG GCGGGCAGCG TGCTCTCCGT CAGCTTCTTC      420
GTGGCCATGC TGGCGCTCAT GGCGGTACTG TACGTCCACA TGCTGGCCCG GGCCTGCCAG      480
CACGGCCGGC ACATCGCCCG GCTCCACAAG ACGCAGCACC CCACCCGCCA GGGCTGCGGC      540
CTCAAGGGCA CGGCCACCCT CACCATCCTG CTGGGCGTCT TCCTCCTCTG CTGGGCACCC      600
TTCTTCCTGC ACCTCTCCCT CGTCGTCCTC TGCCCCCAGC ACCCCACCTG CGGCTGCGTC      660
TTCAAGAACG TCAACCTCTT TCTGGCCCTC GTCATCTGCA ACTCCATC      708
```

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..253
- (D) OTHER INFORMATION:/note= "Fig 1 - Wild Boar"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "X = unknown amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Xaa Pro Asn Gly Leu Phe Leu Ser Leu Gly Leu Val Ser Leu Val Glu

1	5	10	15
Asn Val Leu Val Val Ala Ala Ile Ala Lys Asn Arg Asn Leu His Ser	20	25	30
Pro Met Tyr Tyr Phe Val Cys Cys Leu Ala Val Ser Asp Leu Leu Val	35	40	45
Ser Val Ser Asn Val Leu Glu Thr Ala Val Leu Leu Leu Leu Glu Ala	50	55	60
Gly Ala Leu Ala Ala Gln Ala Ala Val Val Gln Gln Leu Asp Asn Val	65	70	75
Met Asp Val Leu Ile Cys Gly Ser Met Val Ser Ser Leu Cys Phe Leu	85	90	95
Gly Ala Ile Ala Val Asp Arg Tyr Val Ser Ile Phe Tyr Ala Leu Arg	100	105	110
Tyr His Ser Ile Val Thr Leu Pro Arg Ala Gly Arg Ala Ile Ala Ala	115	120	125
Ile Trp Ala Gly Ser Val Leu Ser Ser Thr Leu Phe Ile Ala Tyr Tyr	130	135	140
His His Thr Ala Val Leu Leu Gly Leu Val Ser Phe Phe Val Ala Met	145	150	155
Leu Ala Leu Met Ala Val Leu Tyr Val His Met Leu Ala Arg Ala Cys	165	170	175
Gln His Gly Arg His Ile Ala Arg Leu His Lys Thr Gln His Pro Thr	180	185	190
Arg Gln Gly Cys Gly Leu Lys Gly Ala Ala Thr Leu Thr Ile Leu Leu	195	200	205
Gly Val Phe Leu Leu Cys Trp Ala Pro Phe Phe Leu His Leu Ser Leu	210	215	220
Val Val Leu Cys Pro Gln His Pro Thr Cys Gly Cys Val Phe Lys Asn	225	230	235
Val Asn Leu Phe Leu Ala Leu Val Ile Cys Asn Ser Ile	245	250	

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..253
- (D) OTHER INFORMATION:/note= "Fig 1 - Meishan"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "X = Unknown amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Xaa Pro Asn Gly Leu Phe Leu Ser Leu Gly Leu Val Ser Leu Val Glu
1 5 10 15
Asn Val Leu Val Val Ala Ala Ile Ala Lys Asn Arg Asn Leu His Ser
20 25 30
Pro Met Tyr Tyr Phe Val Cys Cys Leu Ala Val Ser Asp Leu Leu Val
35 40 45
Ser Val Ser Asn Met Leu Glu Thr Ala Val Leu Pro Leu Leu Glu Ala
50 55 60
Gly Ala Leu Ala Ala Gln Ala Ala Val Val Gln Gln Leu Asp Asn Val
65 70 75 80
Met Asp Val Leu Ile Cys Gly Ser Met Val Ser Ser Leu Cys Phe Leu
85 90 95
Gly Ala Ile Ala Val Asp Arg Tyr Val Ser Ile Phe Tyr Ala Leu Arg
100 105 110
Tyr His Ser Ile Val Thr Leu Pro Arg Ala Gly Arg Ala Ile Ala Ala
115 120 125
Ile Trp Ala Gly Ser Val Leu Ser Ser Thr Leu Phe Ile Ala Tyr Tyr
130 135 140
His His Thr Ala Val Leu Leu Gly Leu Val Ser Phe Phe Val Ala Met
145 150 155 160
Leu Ala Leu Met Ala Val Leu Tyr Val His Met Leu Ala Arg Ala Cys
165 170 175
Gln His Gly Arg His Ile Ala Arg Leu His Lys Thr Gln His Pro Thr
180 185 190
Arg Gln Gly Cys Gly Leu Lys Gly Ala Ala Thr Leu Thr Ile Leu Leu
195 200 205
Gly Val Phe Leu Leu Cys Trp Ala Pro Phe Phe Leu His Leu Ser Leu
210 215 220
Val Val Leu Cys Pro Gln His Pro Thr Cys Gly Cys Val Phe Lys Asn

225

230

235

240

Val Asn Leu Phe Leu Ala Leu Val Ile Cys Asn Ser Ile
 245 250

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..253
- (D) OTHER INFORMATION:/note= "Fig 1 - Largewhite and Hampshire"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "X = unknown amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Xaa	Pro	Asn	Gly	Leu	Phe	Leu	Ser	Leu	Gly	Leu	Val	Ser	Leu	Val	Glu	1	5	10	15
Asn	Val	Leu	Val	Val	Ala	Ala	Ile	Ala	Lys	Asn	Arg	Asn	Leu	His	Ser	20	25	30	
Pro	Met	Tyr	Tyr	Phe	Val	Cys	Cys	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	35	40	45	
Ser	Val	Ser	Asn	Val	Leu	Glu	Thr	Ala	Val	Leu	Leu	Leu	Leu	Glu	Ala	50	55	60	
Gly	Ala	Leu	Ala	Ala	Gln	Ala	Ala	Val	Val	Gln	Gln	Leu	Asp	Asn	Val	65	70	75	80
Met	Asn	Val	Leu	Ile	Cys	Gly	Ser	Met	Val	Ser	Ser	Leu	Cys	Phe	Leu	85	90	95	
Gly	Ala	Ile	Ala	Val	Asp	Arg	Tyr	Val	Ser	Ile	Phe	Tyr	Ala	Leu	Arg	100	105	110	
Tyr	His	Ser	Ile	Val	Thr	Leu	Pro	Arg	Ala	Gly	Arg	Ala	Ile	Ala	Ala	115	120	125	
Ile	Trp	Ala	Gly	Ser	Val	Leu	Ser	Ser	Thr	Leu	Phe	Ile	Ala	Tyr	Tyr	130	135	140	

His His Thr Ala Val Leu Leu Gly Leu Val Ser Phe Phe Val Ala Met
 145 150 155 160
 Leu Ala Leu Met Ala Val Leu Tyr Val His Met Leu Ala Arg Ala Cys
 165 170 175
 Gln His Gly Arg His Ile Ala Arg Leu His Lys Thr Gln His Pro Thr
 180 185 190
 Arg Gln Gly Cys Gly Leu Lys Gly Ala Ala Thr Leu Thr Ile Leu Leu
 195 200 205
 Gly Val Phe Leu Leu Cys Trp Ala Pro Phe Phe Leu His Leu Ser Leu
 210 215 220
 Val Val Leu Cys Pro Gln His Pro Thr Cys Gly Cys Val Phe Lys Asn
 225 230 235 240
 Val Asn Leu Phe Leu Ala Leu Val Ile Cys Asn Ser Ile
 245 250

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..253
- (D) OTHER INFORMATION:/note= "Fig 1 - Duroc"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "X = unknown amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Xaa Pro Asn Gly Leu Phe Leu Ser Leu Gly Leu Val Ser Leu Val Glu
 1 5 10 15
 Asn Val Leu Val Val Ala Ala Ile Ala Lys Asn Arg Asn Leu His Ser
 20 25 30
 Pro Met Tyr Tyr Phe Val Cys Cys Leu Ala Val Ser Asp Leu Leu Val
 35 40 45
 Ser Val Ser Asn Val Leu Glu Thr Ala Val Leu Leu Leu Glu Ala
 50 55 60

Gly	Ala	Leu	Ala	Ala	Gln	Ala	Ala	Val	Val	Gln	Gln	Leu	Asp	Asn	Val	
65					70					75					80	
Met	Asp	Val	Leu	Ile	Cys	Gly	Ser	Met	Val	Ser	Ser	Leu	Cys	Phe	Leu	
			85						90					95		
Gly	Ala	Ile	Ala	Val	Asp	Arg	Tyr	Val	Ser	Ile	Phe	Tyr	Ala	Leu	Arg	
			100					105					110			
Tyr	His	Ser	Ile	Val	Thr	Leu	Pro	Arg	Val	Gly	Arg	Ala	Ile	Ala	Ala	
		115					120					125				
Ile	Trp	Ala	Gly	Ser	Val	Leu	Ser	Ser	Thr	Leu	Phe	Ile	Ala	Tyr	Tyr	
	130					135					140					
His	His	Thr	Ala	Val	Leu	Leu	Gly	Leu	Val	Ser	Phe	Phe	Val	Ala	Met	
145					150					155					160	
Leu	Ala	Leu	Met	Ala	Val	Leu	Tyr	Val	His	Met	Leu	Ala	Arg	Ala	Cys	
				165					170					175		
Gln	His	Gly	Arg	His	Ile	Ala	Arg	Leu	His	Lys	Thr	Gln	His	Pro	Thr	
			180					185					190			
Arg	Gln	Gly	Cys	Gly	Leu	Lys	Gly	Thr	Ala	Thr	Leu	Thr	Ile	Leu	Leu	
		195					200					205				
Gly	Val	Phe	Leu	Leu	Cys	Trp	Ala	Pro	Phe	Phe	Leu	His	Leu	Ser	Leu	
	210					215					220					
Val	Val	Leu	Cys	Pro	Gln	His	Pro	Thr	Cys	Gly	Cys	Val	Phe	Lys	Asn	
225					230					235					240	
Val	Asn	Leu	Phe	Leu	Ala	Leu	Val	Ile	Cys	Asn	Ser	Ile				
			245						250							

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATGAGAGGCG	CTCGCCGCGC	CTGGGATTTT	CTCTTCGTCC	TGCAGCTCTT	GCTTCGCGTC	60
CAGACAGGCT	CTTCTCAGCC	ATCTGTGAGT	CCAGAGGAAC	TGTCTCCACC	ATCCATCCAT	120
CCAGCAAAAT	CAGAGTTAAT	CGTCAGTGCT	GGCGATGAGA	TTAGGCTGTT	CTGCACCGAT	180

CCAGGATCTG	TCAAATGGAC	TTTTGAGACC	CTGGGTCAGC	TGAGTGAGAA	TACACACGCA	240
GAGTGGATCG	TGGAGAAAGC	AGAGGCCATG	AATACAGGCA	ATTATACATG	CACCAATGAA	300
GGCGGTTTAA	GCAGTTCCAT	TTATGTGTTT	GTTAGAGATC	CTGAGAAGCT	TTTCCTCGTC	360
GACCCTCCCT	TGTATGGGAA	GGAGGACAAT	GACGCGCTGG	TCCGATGTCC	TCTGACGGAC	420
CCAGAGGTGA	CCAATTACTC	CCTCACGGGC	TGCGAGGGGA	AACCCCTTCC	CAAGGATTTG	480
ACCTTCGTCTG	CGGACCCCAA	GGCCGGCATC	ACCATCAGAA	ACGTGAAGCG	CGAGTATCAT	540
CGGCTCTGTC	TCCACTGCTC	CGCCAACCAG	GGGGGCAAGT	CCGTGCTGTC	GAAGAAATTC	600
ACCCTGAAAG	TGAGGGCAGC	CATCAGAGCT	GTACCTGTTG	TGGCTGTGTC	CAAAGCAAGC	660
TACCTTCTCA	GGGAAGGGGA	GGAATTTGCC	GTGATGTGCT	TGATCAAAGA	CGTGTCTAGT	720
TCCGTGGACT	CCATGTGGAT	CAGGGAGAAC	AGCCAGACTA	AAGCACAGGT	GAAGAGGAAT	780
AGCTGGCATC	AGGGTGACTT	CAATTTTCTG	CGGCAGGAAA	GGCTGACAAT	CAGCTCAGCA	840
AGAGTTAATG	ATTCTGGCGT	GTTTCATGTGT	TACGCCAATA	ATACTTTTGG	ATCTGCAAAT	900
GTCACAACCA	CCTTAGAAGT	AGTAGATAAA	GGATTCAATTA	ATATCTTCCC	TATGATGAAT	960
ACCACTGTGT	TTGTAAACGA	TGGAGAGGAT	GTGGATCTAA	TTGTTGAGTA	CGAGGCGTAC	1020
CCCAAACCTG	AACACCGACA	GTGGATATAT	ATGAACCGCA	CTGCCACTGA	TAAGTGGGAG	1080
GATTATCCCA	AGTCTGAGAA	TGAAAGTAAC	ATCAGATATG	TAAGTGAAC	TCACTTGACC	1140
AGATTAAAAG	GGACCGAAGG	AGGCACCTAC	ACATTTCTCG	TGTCCAATGC	TGATGTCAAT	1200
TCTTCTGTGA	CATTTAATGT	TTACGTGAAC	ACAAAACCAG	AAATCCTGAC	TCATGACAGG	1260
CTCATGAACG	GCATGCTCCA	GTGTGTGGCG	GCAGGCTTCC	CAGAGCCCAC	CATCGATTGG	1320
TATTTCTGTC	CAGGCACCGA	GCAGAGATGT	TCCGTTCCCG	TTGGGCCAGT	GGACGTGCAG	1380
ATCCAAAAC	CATCTGTATC	ACCGTTTGGA	AAACTAGTGA	TTCACAGCTC	CATTGATTAC	1440
AGTGCATTCA	AACACAACGG	CACGGTGGAG	TGCAGGGCTT	ACAACGATGT	GGGCAAGAGT	1500
TCTGCCTTTT	TTAACTTTGC	ATTTAAAGAA	CAAATCCATG	CCCACACCCT	CTTCACGCCT	1560
TTGCTGATTG	GTTTTGTGAT	CGCAGCGGGT	ATGATGTGTA	TCATCGTGAT	GATTCTCACC	1620
TATAAATATC	TACAGAAGCC	CATGTATGAA	GTACAGTGGA	AGGTTGTCTGA	GGAGATAAAT	1680
GGAAACAATT	ATGTCTACAT	AGACCCAACG	CAACTTCCTT	ATGATCACAA	ATGGGAATTT	1740
CCCAGGAACA	GGCTGAGTTT	TGGCAAAACC	TTGGGTGCTG	GCGCCTTCGG	GAAAGTCGTT	1800
GAGGCCACTG	CATACGGCTT	AATTAAGTCA	GATGCGGCCA	TGACCGTTGC	CGTGAAGATG	1860
CTCAAACCAA	GTGCCCATTT	AACGGAACGA	GAAGCCCTAA	TGTCTGAACT	CAAAGTCTTA	1920

AGTTACCTCG	GTAATCACAT	GAATATTGTG	AATCTTCTCG	GCGCCTGCAC	CATTGGAGGG	1980
CCCACCTTGG	TCATTACAGA	ATATTGTTGC	TATGGTGATC	TCCTGAATTT	TTTGAGACGG	2040
AAACGTGATT	CGTTTATTTG	CTCAAAGCAG	GAAGATCACG	CAGAAGCGGC	GCTTTATAAG	2100
AACCTTCTGC	ATTCAAAGGA	GTCTTCCTGC	AGTGACAGTA	CTAACGAGTA	CATGGACATG	2160
AAACCCGGAG	TGTCTTATGT	GGTACCAACC	AAGGCAGACA	AAAGGAGATC	TGCGAGAATA	2220
GGCTCATACA	TAGAACGAGA	TGTGACTCCT	GCCATCATGG	AAGATGATGA	GTTGGCCCTA	2280
GACCTGGAGG	ACTTGCTCAG	CTTTTCTTAC	CAAGTGGCAA	AGGGCATGGC	CTTCCTCGCC	2340
TCGAAGAATT	GTATTACAG	AGACTTGGCG	GCCAGAAATA	TCCTCCTTAC	TCATGGTCGA	2400
ATCACAAAGA	TTTGTGATTT	TGGTCTAGCC	AGAGACATCA	AGAATGATTC	TAATTACGTG	2460
GTCAAAGGAA	ACGCTCGGCT	ACCCGTGAAG	TGGATGGCAC	CTGAGAGCAT	TTTCAACTGT	2520
GTCTACACAT	TTGAAAGCGA	TGTCTGGTCC	TATGGGATTT	TTCTGTGGGA	GCTCTTCTCT	2580
TTAGGGAGCA	GCCCCTACCC	CGGAATGCCA	GTTGATTCTA	AATTCTACAA	GATGATCAAG	2640
GAGGGTTTCC	GAATGCTCAG	CCCTGAGCAT	GCACCTGCGG	AAATGTATGA	CATCATGAAG	2700
ACTTGCTGGG	ATGCGGATCC	CCTCAAAAGA	CCAACGTTTA	AGCAGATCGT	GCAGCTGATT	2760
GAGAAGCAGA	TTTCGGAGAG	CACCAATCAC	ATTTATTCCA	ACTTAGCGAA	CTGCAGCCCC	2820
CACCGGGAGA	ACCCGCGGGT	GGATCATTCT	GTGCGGATCA	ACTCCGTGGG	CAGCAGTGCC	2880
TCCTCCACGC	AGCCTCTGCT	TGTCCACGAA	GATGTCTGA			2919

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CTGCAGTGCT	CCTGGTGAGG	GGGGACGGGC	GCTGGAGCCA	GGCTGCGGGG	CTGAGGGCAG	60
TGGTGCCGTC	CTGCGGCCCC	GTTCTTACGT	GGCTGGGCAG	CCCCTTGGCA	GAGAGGACGG	120
GCCGGACATC	TCTGAAGGTA	TGGACGCTGG	ACCCTCTGGG	GCCCGACAGA	GGAAGAGCCA	180
GCACTTCCAG	GAGGCATGGG	GAGTGGGGGA	GGCTGGAGAG	ACGGCGGGGA	GCGCCACCTC	240

CATCCAGAGA CCACCACGCC CGCCTTTGGG GCGCGCTCTG GGGACTTTGC CCCCCACTGG	300
GGTGGGACGT GTGCGGGCAG AAGCTGTCCG GGTGTTGCTC ACTGCAGGAC CTCAGGGGAA	360
GGCCTTCGTG ACTGCTAGGA AGCAGGCGCA GCGCCCCGGC GGAGGGCGGG GCCCCTCTCT	420
TCTACGGCTC AGTG	434

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CTGCAGTGCT CCTGGTGAGG GGGGCGGGCG CTGGAGCCAG GCTGCGGGGC TGAGGGCAGT	60
GGTGCCGTCC TGCGGCCCGG TTCCTACGTG GCTGGGCAGC CCCTTGGCAG AGAGGACGGG	120
CCGGACATCT CTGAAGGTAT GGACGCTGGA CCCTCTGGGG CCCGACAGAG GAAGAGCCGG	180
CACTTCCAGG AGGCATGGGG AGTGGGGGAG GCTGGAGAGA CGGCGGGGAG CGCCACCTCC	240
ATCCAGAGAC CACCACGCCC GCCTTTGGGG GCGCGCTCTGG GGACTTTGCC CCCCCACTGGG	300
GTGGGACGTG TGCGGGCAGA AGCTGTCCGG GTGTTGCTCA CTGCAGGACC TCAGGGGAAG	360
GCCTTCGTGA CTGCTAGGAA GCAGGCGCAG CGCCCCGGCG GAGGGCGGGG CCCCTCTCTT	420
CTACGGCTCA GTG	433

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CTGCAGTGCT CCTGGTGAGG GGGGACGGGC GCTGGAGCCA GGCTGCGGGG CTGAGGGCAG	60
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TGGTGCCGTC	CTGCGGCCCC	GTTCCCTACGT	GGCTGGGCAG	CCCCTTGGCA	GAGAGGACGG	120
GCCGGACATC	TCTGAAGGTA	TGGACGCTGG	ACCCTCTGGG	GCCCGACAGA	GGAAGAGCCG	180
GCAC'TTCCAG	GAGGCATGGG	GAGTGGGGGA	GGCTGGAGAG	ACGGCGGGGA	GCGCCACCTC	240
CATCCAGAGA	CCACCACGCC	CGCCTTTGGG	GCGCGCTCTG	GGGACTTTGC	CCCCCACTGG	300
GGTGGGACGT	GTGCGGGCAG	AAGCTGTCCG	GGTGT'TGCTC	ACTGCAGGAC	CTCAGGGGAA	360
GGCCTTTCGTG	ACTGCTAGGA	AGCAGGCGCA	GCGCCCCGGC	GGAGGGCGGG	GCCCC'TCTCT	420
TCTACGGGCTC	AGTG					434

NOTES